

*AMENDMENTS TO THE SPECIFICATION*

Please insert the following new paragraphs at page 4, after line 27:

Figure 2 shows the predicted secondary structure of preproNPY mRNA and the predicted structure of the 5' end (1 to 138 bases) of the full preproNPY mRNA sequence published in GenBank Accession No. K01911. The secondary structure was predicted by using the MFOLD program of the Genetics Computer Group of the University of Wisconsin. Squiggle plot of: osa1.mfold February 7, 19100 12:46. (Linear) MFOLD of: osa1.seqT: 37.0 Check: 5173 from: 1 to: 138 February 7, 19100 12:43. Length 138 Energy -28.4. The nucleotide sequence “acaagcgacugg” is the wildtype sequence of SEQ ID NO:7.

Figure 3 shows the predicted secondary structure of mutated preproNPY mRNA and the predicted structure of the 5' end (1 to 138 bases) of the full mutated preproNPY mRNA sequence published in GenBank Accession No. K01911. The secondary structure was predicted by using the MFOLD program of the Genetics Computer Group of the University of Wisconsin. The mutated base T to C is base number 106. Squiggle plot of: osa2.mfold February 7, 19100 14:11. (Linear) MFOLD of: osa2.seqT: 37.0 Check: 4340 from: 1 to: 138 February 7, 19100 14:07. Length 138 Energy -26.4 -28.4. The nucleotide sequence “acaagcgaccgg” is the mutant sequence of SEQ ID NO:7.

Please delete pages 10 and 11 of the specification containing Schemes 1 and 2.

Please amend the first paragraph on page 8 to read as follows.

The influence of the mutated NPY gene is preferably counteracted by using a short, allele specific oligonucleotide, which includes the sequence of the mutated part: ... cga ct/cg ggg ... (SEQ ID NO:8). This can be accomplished by using oligonucleotides of various lengths, but all recognizing the mutated base sequence. According to the predicted secondary structure of preproNPY mRNAs (~~Schemes 1 and 2~~ Figs. 2 and 3), the best target sequence is between -9 and +2 bases around the mutation, i.e., a sequence targeting to ~~3'-ac aag cga ctg g-5'~~ 5'-ac aag cga ccg g-3' (SEQ ID NO:9). This sequence contains 'bulbs' which are known to enhance the binding of oligonucleotide to the target mRNA.